

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus.p2n model

Run on: February 23, 2003, 12:05:44 : Search time 74 Seconds

(without alignments)
4242.654 Million cell updates/sec

Title: US-09-804-014A-8

Perfect score: 2918
Sequence: 1 MERRRGTSGRKGKDGKDPG.....VPELPPIAPMAPREHLVTEV 559

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delpop 6.0 , Delpext 7.0	

Searched: 442118 seqs, 280819700 residues

Total number of hits satisfying chosen parameters: 884236

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7

Database : Published_Applications_NA:*

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10:	/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/2/pubpna/US10_NEM_PUB.seq:*
12:	/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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14:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2807.5	96.2	6823	9	US-09-989-920-16
2	2801.5	96.0	4372	10	US-09-993-811-1
3	2418	82.9	1792	10	US-09-974-712-3
4	2320	79.5	1371	10	US-09-974-712-1

	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
	2218.5	2210.5	2210.5	1447.5	1447.5	735.5	728	728	725.5	651.5	649.5	649.5	638	611.5	600	585	585	578	564	564	564	496	478.5	416	390.5	278.5	276.5	247	240	237	236.5	235.5	228.5	228	226	222	220.5	216	215	210.5	210.5	
	76.0	75.8	75.8	49.6	49.6	25.2	24.9	24.9	24.9	22.3	22.3	22.3	21.9	21.0	20.6	20.0	20.0	19.8	19.3	19.3	17.0	16.4	14.3	13.4	9.5	9.5	8.5	8.2	8.1	8.1	8.1	7.8	7.7	7.6	7.6	7.4	7.4	7.2	7.2	7.2		
	3474	1599	3473	2867	2867	2847	2064	2121	1917	1844	1468	2483	522	2127	1278	998	1979	1340	492	492	706	1668	607	1148	2028	380	2821	3074	612	3287	1887	3111	2169	9	2772	900	900	735	2565	2667	2694	3071
	US-09-993-811-11	US-09-993-811-4	US-09-993-811-5	US-09-954-436-1227	US-09-880-107-2354	US-10-024-623-10	US-10-062-879-3	US-10-062-879-3	US-10-024-623-12	US-10-016-647-3	US-09-993-811-8	US-10-143-002-3	US-09-993-811-7	US-10-143-002-1	US-10-016-647-1	US-09-864-761-1804	US-09-864-761-3784	US-09-864-761-20550	US-09-989-442-11	US-09-989-442-11	US-09-989-442-11	US-09-993-811-3	US-09-993-811-13	US-09-864-761-18555	US-09-822-849A-405	US-09-840-125-1	US-09-960-352-331	US-09-880-107-3358	US-09-813-148-1	US-09-864-761-26504	US-10-128-870-19	US-09-825-147-3	US-10-128-870-22	US-10-128-870-3	US-09-825-147-1	US-10-128-870-5	US-10-128-870-7	US-10-128-870-26	US-09-810-796-3	US-09-810-796-2	US-09-810-796-1	
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ALIGNMENTS

RESULT 1
US-09-989-920-16
: Sequence 16, Application US/0989920
: Patent No. US20020172957A1
: GENERAL INFORMATION:
: APPLICANT: Macina, Roberto
: APPLICANT: Macina, Roberto
: APPLICANT: Chen, Sel-yu
: APPLICANT: Sun, Yonnging
: APPLICANT: Liu, Chenghua
: TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and :
: FILE REFERENCE: DEX-0291
: CURRENT APPLICATION NUMBER: US/09/989,920
: PRIOR FILING DATE: 2001-11-21
: PRIOR APPLICATION NUMBER: 60/252,500
: NUMBER OF SEQ ID NOS: 284
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 16
: LENGTH: 6823
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-989-920-16
Alignment Scores:
Pred. No.: 3,38e-194 Length: 6823
Score: 2807.50 Matches: 553
Percent Similarity: 96.35% Conservative: 2

OY		1	MetGluArgAlaGlyThrGlySerPheArgIleuInsAspGluValuysGIyASpProgly	20
Db		5	TTGGAGAGACCACAGACAGATCCCGCGCAGAAAGCAGAGAGAANAAGGACCCC	64
OY		21	ThreGLysAlaGlnSerArgArgGlyValArgArgArgArgGlyArgAlaGlyArgA	40
Db		65	ACGGGAAGAGCGCAGAGACGCAGCGGCGCGCGCGCGGCGAGCGAGCGCGGCG	128
OY		41	SerArgGlnArgAlaArgGlyValArgProValAlaLeuArgProAlaGlyValThValPro	60
Db		125	TTCGGCGAGAGGGCGCGGGGTGCCCTTCCCTCCGCCCGCGGGGTCAAGTGCC	184
OY		61	ProPheSerArgProSerArgProAlaGlyLeu-PheTryAlaArgTrpProAspThrGl	80
Db		185	CCTCCCTGGCCCTTAGCGCGGCTTGCGGGGTATTTTTACCGCGGACCCGACACCG	244
OY		80	YHisArgAlaGlyAlaAla-----	86
Db		245	ACACCGGGCTGTGGGGCGG- GCGCGCGCGCGCGAGCGCGCCGAGCGCGCGCACCGG	304
OY		87	-----ValGlyAlaTrpArgArgPheAlaGlyArgArgGlyCysAlaArgHISgLYAL	104
Db		304	GCCGGGCGCTCCGGGGCCACACTCGGTTGCGGGGTGCGGGGGCTGGCGGCCCATGGAGC	364
OY		104	aAlaValProAlaAlaProCysGlyCysCysGlyValArgLeuValLeuAsnValAlaGlyLe	124
Db		364	CGCGGTGCCCCCGC--CGGTGCGGTGTCGAGCGGGGTGTGTCTCAACGTGGCGGGCT	424
OY		124	uArgPheGluThrArgAlaArgTrpLeuGlyValArgPheProAspHrileuLeuGlyAspPr	144
Db		422	GCGCTTCAGACGCGGGCGCCACAGCTGGGGCGGTCCCGGACACTGTGCTAGGGGAGCC	482
OY		144	oAlaArgArgGlyValArgPheTryASPaspAlaArgArgGlyLurArgPhePheAspArgHSAR	164
Db		482	AGCGGCGCGGGCGGCTCTACAGACAGCGCGCGCGAGATTTCTTCGACCGCGACCG	544
OY		164	gProSerPheAspAlaValLeuTryTYRTrpGlnSerGlyGlyValArgLeuArgArgProAl	184
Db		542	GCCAGGCTTCAGCGCGCGGTCTACTACTACAGCTCGGGTGGCGGTGCGCGCGCGCGC	604
OY		184	aHisValProLeuAspValPheLeuGlnGluValAlaPheTryGlyLeuGlyAlaAlaAl	204
Db		602	GCACGTGCGGCTGCACAGCTTCTCTCGAAGAGAGTGGCTTCTACGGGCTGGCGGGCGC	664
OY		204	aLeuAlaArgLeuArgGlnAspGluGlyCysProValProBrogLuArgProLeuProAr	224
Db		662	CCTGGCACGCGCTGGCGGAGCAGAGGGGTGCCGTGGCGCGCCGACGCCCCCTGCCCG	724
OY		224	gArgAlaPheAlaArgGlnLeuTrpLeuLeuPheGlnPheProGlnSerSerGlnAlaAl	244
Db		722	CCGGGCTTTCGCGCGCACGCTGTGTGGCTTTTGAGTTTTCCGAGAGCTTCAAGGCGC	784
OY		244	aArgValLeuAlaValAlaSerValLeuValIleLeuValSerIleValValPheCysLe	264
Db		782	GCGGTGTCTCCGAGTCTCCGHTGTGTATCTGTCATCTGTCAMCGHCGHCTTGTGCT	844
OY		264	uGluThrIleuProAspPheArgAspAspArgAspGlyThrGlyLeuAlaAlaAlaAlaAl	284
Db		842	CGAGCGGTGCTGACTTCGCGCAGACGCGGACGCGGCGGCTTCTGCTGCAGCGCGC	904
OY		284	aAlaGlyProValPheProAlaProLeuAsnGlySerSerGlnMetProGlyAsnPropR	304
Db		902	AGCGGGCGCG---TTCCCGCGTCCGCTGAAGGCTCCAGCCAATGCTGTGAATAATCAC	954
OY		304	cArgLeuProPheAsnAspProPhePheValValGluThrLeuCysIleCysTrpPheSe	324

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RESULT 3
US-09-974-712-3
; Sequence 3, Application US/09974712
; Patent No. US20020119540A1
; GENERAL INFORMATION:
; APPLICANT: Fridgley, Carl Johan
; APPLICANT: Hilbun, Erin
; APPLICANT: Gerhardt, Brenda
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020119540A1 Human Ion Channel Protein and Polynucleo
; FILE REFERENCE: LEX-0251-USA
; CURRENT APPLICATION NUMBER: US/09/974,712
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/239,623
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1792
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-974-712-3

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Alignment Scores:

Pred. No.:	1,12e-166	Length:	1792
Score:	2418.00	Matches:	473
Percent Similarity:	97.93%	Conservative:	1
Best Local Similarity:	97.73%	Mismatches:	5
Query Match:	82.86%	Indels:	6
DB:	10	Gaps:	2

US-09-804-014a-8 (1-559) x US-09-974-712-3 (1-1792)

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QY 80 GlyHsArgAlaGlyAlaAla-----ValGlyAlaThrArgArgPheAlaGly 95
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Db 14 GCGGCGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 73
QY 96 ArgArgGlyCysAlaArgHisGlyAlaAlaValProAlaAlaProCysGlyCysGlu 115
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 131
QY 116 ArgLeuValLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGlyArg 135
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 132 CCGCTGCTGCTCAACCTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 191
QY 136 PheProAspThrLeuLeuGlyAspProAlaArgArgGlyArgPheTyrAspAlaArg 155
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Db 192 TTCGCGGACACTGCTGAGGAGACCGAGCGCGCGCGCGGCGGCTTCTACGACGCGGCG 251
QY 156 ArgGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyrGln 175
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Db 252 CCGGAGTATTTCTTCACCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 311
QY 176 SerGlyGlyArgLeuArgArgProAlaHisValProLeuAspValPheLeuGluGluVal 195
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 312 TCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 371
QY 196 AlaPheTyrGlyLeuGlyAlaAlaAlaLeuAlaArgLeuArgGluAspGluCysPro 215
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 372 GCGTCTTACGCGGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 431
QY 216 ValProProGluArgProLeuProArgArgAlaPheAlaArgGluLeuPheLeuPhe 235
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 432 GCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 491
QY 236 GluPheProGluSerSerGlnAlaAlaAlaArgValLeuAlaValSerValLeuValLe 255
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Db 492 GAGTTTCCGAGAGCTCTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 551
QY 256 LeuValSerIleValAlaPheCysLeuGluThrLeuProAspPheArgAspAspArg 275
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QY 276 GlyThrGlyLeuAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGly 295
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QY 296 SerSerGlnMetProGlyAsnProProArgLeuProPheAsnAspProPhePheVal 315
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Db 669 TCCAGGCAAAATGCTGGAATCCACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 728
QY 316 GluThrLeuCysIleCysTrrPheSerPheGluLeuLeuValArgLeuLeuValCysPro 335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 729 GAGAGCGCTGTGTATTTGTGTCTTCCTTTCGAGCTGCTGTGCGCTCTGCTGTGTCCA 788
QY 336 SerIlyAlaIlePhePheIysAsnValMetAsnLeuIleAspPheValAlaIleLeuPro 355
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 789 ACCAAGGCTATCTTCTTCAAGAACGATGAACCTCATGATTTGTGGCTATCTCTCC 848
QY 356 TyrPheValAlaLeuGlyThrGluLeuAlaArgGlnArgGlyValGlyGlnGlnAlaMet 375
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Db 849 TACTTTGTGGCACTGGGACCGACGAGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 908
QY 376 SerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgIlePheIysLeuSer 395
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 909 TCACTGGCATCTGAGAGATCCGATTCGATTTGGTGTCTTCGCGCATCTTCAAGCTGTCC 968
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QY 396 ArgHisSerIlyGlyLeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetArgGluLeu 415
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Db 969 CCGCACTCAAAAGGCGCTGCAAAATCTTGGGCGGAGCGCTTGGGCGGCGGCGGCGGCGG 1028
QY 416 GlyLeuIleIlePhePheLeuPheIleGlyValAlaLeuPheSerSerAlaValTyrPhe 435
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Db 1029 GCGCTCCTCATCTTTTCTCTTCCTTCATCGGTGTGGTCTCTTTTCCAGCGCGCTACTTT 1088
QY 436 AlaGluValAspArgValAspSerHisPheThrSerIleProGluSerPheTrrPala 455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1089 GCCGAAGTTGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1148
QY 456 ValValThrMetThrThrThrValGlyTyrGlyAspMetAlaProValThrValGlyLys 475
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1149 GTATGTACCATGACTTACATGCTGTAGGAGACATGGACCGGCTGCTGGGTGGCAAG 1208
QY 476 IleValGlySerLeuCysAlaIleAlaGlyValLeuThrIleSerLeuProValProVal 495
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1209 ATATGTGGGCTGTGTGTGCTCATTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1268
QY 496 IleValSerAsnPheSerTyrPheTyrHisArgGluThrGluGlyGluGluAlaGlyMet 515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1269 ATTGTCTCCAAATTTACGCTACTTTATCACCGGAGACAGAGGCGGAGAGCGCTGGAGTG 1328
QY 516 PheSerHisValAspMetGlnProCysGlyProLeuGluGlyLysAlaAsnGlyLysLeu 535
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1329 TTCAGCATGTGAGCATGACATGCGCTTGTGGCCACTGGAAGGCAAGCCATGGGGCGCTG 1388
QY 536 ValAspGlyGluValProGluLeuProProProLeuTrrPalaProProArgGluHisLeu 555
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1389 GTGAGCGGGGAGGATGACTGAGCTACACCTCCACTGTGGCGACCCCGCAAGAAACACTG 1448
QY 556 ValThrGluVal 559
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Db 1449 GTACACCGAAGTG 1460

RESULT 4
US-09-974-712-1
; Sequence 1, Application US/09974712
; Patent No. US20020119540A1
; GENERAL INFORMATION:
; APPLICANT: Fiddle, Carl Johan
; APPLICANT: Hilpun, Erin
; APPLICANT: Gerhard, Brenda
; APPLICANT: Turner, C. Alexander Jr
; TITLE OF INVENTION: NO. US20020119540A1e1 Human Ion Channel protein and Polynucleo
; FILE REFERENCE: LEX-0251-USA
; CURRENT APPLICATION NUMBER: US/09/974,712
; PRIOR APPLICATION NUMBER: 2001-10-10
; PRIOR FILING DATE: US 60/239,623
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1371
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-974-712-1

Alignment Scores:
Pred. No.: 1.02e-159 Length: 1371
Score: 2320.00 Matches: 452
Percent Similarity: 99.12% Conservative: 1
Best Local Similarity: 98.91% Mismatches: 3
Query Match: 79.51% Indels: 2
DB: 10 Gaps: 1

US-09-804-014a-8 (1-559) x US-09-974-712-1 (1-1371)
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Db 3 GAGCGCGCGGTGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 60
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QY 123 GLEuNArpHeGluThrArGAlArGThrLeuGlyArGpHeProAspThrLeuGly 142
DB 61 GGGGTGGCTTCAGAGCGGGCGCGACGCTGGCGCTCCGAGACACTCTCAGG 120
QY 143 AspProAlaArGArGgLyArGpHeTyAspAspAlaArGArGgLyUrTyPheAspArG 162
DB 121 GACCACGGCGCGCGCGCTTCTACGACGCGCGCGCGAGTATTCTTGACCGG 180
QY 163 HisArProSerPheAspAlaValLeuTyTyTyGlnSerGlyGlyArGLeuArG 182
DB 181 CACCGGCCAGCTCGAGCGCGCTCTACTACTACAGTCCGCTGGGGCGCTCGGGG 240
QY 183 ProAlaHisValProLeuAspValPheLeuGlnUValAlaPheTyTyGlyLeuGlyAla 202
DB 241 CCGCGCAGCTGGCGCTCGAGCTCTCTGAAAGAGTGGCGCTTACGGGCTGGCGG 300
QY 203 AlaAlaLeuAlaArGLeuArGgLyAspGlyGlyCysProValProProGluArGProLeu 222
DB 301 GCGGCTTGGACGCGCTGGCGCGAGAGAGGCGTCCCGTGGCGCGCGCGCGCTG 360
QY 223 ProArGArGAlaPheAlaArGgLnLeuTyPheLeuPheGluPheProGluSerSerGln 242
DB 361 CCGCGCGCGCTTCGCGCGCGCGCGCGCTGCTTTCGAGTTCCCGAGAGCTCTCAG 420
QY 243 AlaAlaArGValLeuAlaValSerValLeuValIleLeuValSerIleValValPhe 262
DB 421 GCGCGCGCTGGCTGGCGCGAGTCTCGTCTGCTCATCCGCTCCATCGTCTGCTC 480
QY 263 CysLeuGlnThrLeuProAspPheArGAspAspArGAspGlyThrGlyLeuAlaAla 282
DB 481 TGGCTGAGAGCGCTGCTGACTTCCGCGAGCAGCGCGCGCGCGCTGCTGCTGCA 540
QY 283 AlaAlaAlaGlyProValPheProAlaProLeuAsnGlySerSerGlnMetProGlyAsn 302
DB 541 GCGCGCAGCGCGCGCGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 597
QY 303 ProProArGLeuProPheAsnAspProPhePheValValGlnThrLeuGlyIleCysTrp 322
DB 598 CCAACCGCGCTGCTTCATGAGCGCGCTTCTGCTGGAGAGCGCTGATTTGTTGG 657
QY 323 PheSerPheGlnLeuLeuValArGLeuValCysProSerIleValIlePhePheGly 342
DB 658 TTCTCCTTGAAGCGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
QY 343 AsnValMetAsnLeuIleAspPheValAlaIleLeuProTyPheValAlaLeuGlyThr 362
DB 718 AACGTGATGAACCTCATGATTTGTGCTATCTCTCTACTTTGGGCACTGGGCA 777
QY 363 GlnLeuAlaArGlnArGgLyValGlnGlnAlaMetSerLeuAlaIleLeuArGVal 382
DB 778 GAGTGGCGCGCGCGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 837
QY 383 IleArGLeuValArGValPheArGLePheGlyLeuSerArGHisSerIleGlyLeuGln 402
DB 838 ATCCGATGGGTGGCTGCTTCCGATCTTCAAGCTGTCGCGGCACTGAAGGGCTGCA 897
QY 403 IleLeuGlyIleThrLeuArGAlaSerMetArGgLyLeuGlyLeuLeuIlePhePheLeu 422
DB 898 ATCTGGGCGAGAGCTTCGGCGCTCATGAGTGGGCGCTCCATCTTTTCTCTC 957
QY 423 PheIleGlyValValLeuPheSerSerAlaValTyPheAlaGlnUValAspArGValAsp 442
DB 958 TTCTATCGGTGCTCTCTTTCAGCGCGCTCTACTTGGCGAAGTTGACGGGTGAC 1017
QY 443 SerHisPheThrSerIleProGluSerPheTyPheTyPheAlaValIleThrMetThrVal 462
DB 1018 TCCCATTTCACTACATCCCGATCTCTTCTGCGGGGAGTACACATACATACAGTT 1077
QY 463 GlyTyTyIleAspMetAlaProValThrValGlyGlyIleValGlySerLeuGlyAla 482
DB 1078 GGGTATGAGACATGAGCAGCGCTCATGTGGTGGCAAGATAGGGGCTCTGTGTC 1137

QY 483 IleAlaGlyValLeuThrIleSerLeuProValIleValSerAspPheSerTy 502
DB 1138 ATTGCGGGCTGTGACTATTCTCCGCACTGCGCGCTCATGCTCAATTGCTAC 1197
QY 503 PheTyThsArGgLyThrGlnGlyGlyGlnAlaGlyMetPheSerHisValAspMetGln 522
DB 1198 TTTTATCAGCGGAGACAGAGGCGGAGAGAGGCTGGATGTTTACCATGTGACATGCA 1257
QY 523 ProCysGlyProLeuGlnGlyLysAlaAsnGlyIleLeuValAspGlyGlnUValProGlu 542
DB 1258 CCTTGTGGCCATCGAGAGGCGCAATGCGGGCTGGTGGAGCGGGAGTACTGAG 1317
QY 543 LeuProProLeuTyPheAlaProProArGgLnHisLeuValIleThrGlnVal 559
DB 1318 CTACCACTCTCATCTGGGCGCGCGCGAGGAGAACCTGTGACCGAAGTG 1368
RESULT 5
US-09-993-811-11
; Sequence 11, Application US/09993811
; Patent No. US20020119476A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia AB
; TITLE OF INVENTION: Nucleotide sequences
; FILE REFERENCE: 00248
; CURRENT APPLICATION NUMBER: US/09/993,811
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 11
; LENGTH: 3474
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (497)..(1861)
US-09-993-811-11
Alignment Scores:
Pred. No.: 6,75e-152 Length: 3474
Score: 2218.50 Matches: 454
Percent Similarity: 85.14% Conservative: 10
Best local Similarity: 83.30% Mismatches: 61
Query Match: 76.03% Indels: 21
DB: 10 Gaps: 8
US-09-804-014a-8 (1-559) x US-09-993-811-11 (1-3474)
QY 21 ThrGlyLysAlaGlnSerArGArGgLyArGArGArGArGgLyArGAlaGlyAla 40
DB 268 ACAAGGAAAGTCAAGATCCACGGA-----AAAGCGCGGCTGGCAGTGTCCACA 321
QY 41 SerArGlnArGAlaArGgLyArGProValAlaLeuArGProAlaGlyValThrValPro 60
DB 322 GGTGTGGAAACGCGAGAGGCGCGCT-----AGCCCGGGGGGTAAACCGCC 372
QY 61 ProProSerArGProSerArGProAlaGlyLeuPheTyAla----- 74
DB 373 CCTCCCGCGCGCTGGCGG-----ACTTTCATGCTATTTTACC CGCGCAC 423
QY 75 ArGThrProAspThrGlnHisArGAlaGlyAlaAlaValProAlaAlaProCysGlyCysCys 474
DB 424 CGGACACCGCATGGG-----GGTGGCGGCTGGGGCGCACACGTCCTTACC 474
QY 95 GlyArGArGgLyCysAlaArGHisGlyAlaAlaValProAlaAlaProCysGlyCysCys 114
DB 475 GGTGCGCGCGCTGGCGCGCATGAGCCAGCGTGGCCGCG-----CCGTGGGCTGTGC 532
QY 115 GlnArGLeuValLeuAsnValAlaGlyLeuArGpHeGlyThrArGAlaArGThrLeuGly 134
DB 533 GAGCGGTGTGCTCAACGTGGCGGTGGCTTCAAGACCGCGCGCGACCTGTGGC 592
QY 135 ArGpHeProAspThrLeuLeuGlyAspProAlaArGArGgLyArGpHeTyAspAspAla 154

Db 593 CGTTCCCGGACACGCTGCTGGGGACCCGGTGGCCGACCGCTTCTACGACGGCCG 652
Qy 155 ArgArgGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyr 174
Db 653 CGCCCGGAGTATTTCTTCGACCGACCGCGCCGCTCGATGGCGCTCTACTACTAC 712
Qy 175 GluSerGlyGlyArgLeuArgArgProAlaHisValProLeuAspValPheLeuGlu 194
Db 713 CAGTCGGGGCGCGGCTGAGACGGCGCGACGCTGCCCTCGACGCTTCTCTGAGAG 772
Qy 195 ValAlaPheTyrGlyLeuGlyAlaAlaAlaLeuAlaArgLeuArgGluAspGlyCys 214
Db 773 GTGCTCTTCTACGGGCTGGGG---CGGGGGCTGGCGGGCGCGGAGAGAGAGGCTGC 829
Qy 215 ProValProProGluArgProLeuProArgArgAlaPheAlaArgGluLeuTyrLeu 234
Db 830 GCGGTC---GCCGAGCGCGCGCTGCC---CCGCCCTTGGCGCTGAGCTGCTGCTGC 883
Qy 235 PheGluPheProGluSerSerGlnAlaAlaArgValLeuAlaValSerValLeuVal 254
Db 884 TTGCAATTTCTTGAAGCTGCGAGGCTGCGCGCTGCTGCGCGGTCTCGTACTGTC 943
Qy 255 IleValSerIleValValPheCysLeuGluTyrLeuProAspPheArgAspArg 274
Db 944 ATCTGCTCCATCGTGGCTTTGGCTGAGACACTGCCAGACTTCCGCGACGACCC 1003
Qy 275 AspGlyThrGlyLeuAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsn 294
Db 1004 GATGACCGCGGGCTCGCGCGGTGCTACTGCTGCTCTCGCTCGGCTCAAT 1063
Qy 295 GlySerSerGlnMetProGluAsnProProArgLeuProPheAsnProPhePheVal 314
Db 1064 GGTCTCCAGTCCATGCCAGAGACCCCTCCCGACAGCCCTTCAACGATCTTTGTG 1123
Qy 315 ValGluThrLeuCysIleCysTyrPheSerPheGluLeuValAlaArgLeuValCys 334
Db 1124 GTGAGACCGCTGTATCTGCTGCTGCTGCTGAGAGTGTGCTGCTGCTGCTGCTG 1183
Qy 335 ProSerIleAlaIlePhePhePheValMetAsnLeuIleAspPheValAlaIleLeu 354
Db 1184 CTTAGCAACCTGTCTTCAAGAAATGTATGAACCTAATTAATCTCGGCGCATCTG 1243
Qy 355 ProTyrPheValAlaLeuGlyThrGluLeuAlaArgGlnArgGlyValGlyGlnAla 374
Db 1244 CCTTACTTCTGCGCCCTGGGACGAGGTTAGCCCGAGGGGTGGGCGACCGCGCT 1303
Qy 375 MetSerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgIlePheCys 394
Db 1304 ATGTCCCTGGCCATCTAAGGGTCATCCGATGTGTGCTCTTCCGCACTTCAAGCTC 1363
Qy 395 SerArgHisSerIleGlyLeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetArg 414
Db 1364 TCCAGGCATTTGAAAGGCTACAGATCTTGGTCAGACACTGGGGCTTCCATGCGT 1423
Qy 415 LeuGlyLeuLeuIlePhePheLeuPheIleGlyValValLeuPheSerSerAlaValTyr 444
Db 1424 CTAGGCTCTCTATCTTCTTCTCTTCAATGGGCTGCTCTTCTTCCACGAGCTTAC 1483
Qy 435 PheAlaGluValAspArgValAspSerHisPheThrSerIleProGluSerPheTyr 454
Db 1484 TTGTGAGAGTGAGCGGGTGACACCATTTCCACAGCATCCCGGAGTCTTTTG 1543
Qy 455 AlaValValThrMetThrThrValGlyTyrGlyAspMetAlaProValThrValGly 474
Db 1544 GGAGTGTACCATGACACAGGTTGGCTATGGGGCATGGACCCCTCAACCGGGTGG 1603
Qy 475 LysIleValGlySerLeuGlyAlaIleAlaGlyValLeuThrIleSerLeuProValPro 494
Db 1604 AAGATGCTGGCTCTCTGTGTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1663
Qy 495 ValIleValSerAsnPheSerTyrPheTyrHisArgGluThrGluGlyGluAlaGly 514
Db 1664 GTCATGCTCTTAACCTTAAGCTTAATTACACCGGGAACAGAGGCGCAAGAGGCA 1723

Qy 515 MetPheSerHisValAspMetGlnProCysGlyProLeuGluGlyLysAlaAsnGly 534
Db 1724 ATGTACAGCCATGTGAGACACACAGCCCTGCGGTACCTGAGGGGCAAGGCTAATGG 1783
Qy 535 LeuValAspGlyGluValProGluLeuProProLeuTyrPheAlaProProArgGluHis 554
Db 1784 CTGGTGAGCTCTGAGTGCTTGAAGCTCTCCACACTGTGGCCCTCGAGGGAACAC 1843
Qy 555 LeuValThrGluVal 559
Db 1844 ATGTGAGTGAAGTGTG 1858
RESULT 6
US-09-993-811-4
; GENERAL INFORMATION:
; APPLICANT: Pharmacia AB
; TITLE OF INVENTION: Nucleotide Sequences
; FILE REFERENCE: 00248
; CURRENT APPLICATION NUMBER: US/09/993,811
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; JOURNAL: Journal of Biological Chemistry
; VOLUME: 273-
; ISSUE: 10;
; PAGES: 58515857
; DATE: 1998-03-06/
; DATABASE ACCESSION NUMBER: GenBank/AF032099
; DATABASE ENTRY DATE: 1998-04-04
US-09-993-811-4
Alignment Scores:
Pred. No.: 1,03e-151 Length: 1599
Score: 2210.50 Matches: 452
Percent Similarity: 84.77% Conservative: 10
Best Local Similarity: 82.94% Mismatches: 62
Query Match: 75.75% Indels: 21
DB: Gaps: 9
US-09-804-014a-8 (1-559) x US-09-993-811-4 (1-1599)
Qy 21 ThrGlyLysAlaGlnSerArgArgGlyArgArgArgGlyArgAlaGlyArgAla 40
Db 7 ACAAGGAACCTCAAGATCCACGGA-----AAAGCGCGGGTGACAGTGTTCACA 60
Qy 41 SerArgGlnArgAlaArgGlyArgProValAlaLeuArgProAlaGlyValThrValPro 60
Db 61 GGTGTGGGAACGGCAGAGGGCGCCCT-----AGCCCGCGGGGTAAACACCGCCC 111
Qy 61 ProProSerArgProSerArgProAlaGlyLeuPheTyrAla----- 74
Db 112 CTTCCCGCGCGCGCTGGCCG-----ACTTTCATGCTATTTTTCACCGCGCACAC 162
Qy 75 ArgThrProAspThrGlyHisArgAlaGlyAlaAlaValAlaThrArgArgPheAla 94
Db 163 CGGACACCGGACGAGGGT-----GGCTGGCGGCTGGGGCCACAGCTCGCTTCACC 213
Qy 95 GlyArgArgGlyCysAlaArgHisGlyAlaAlaValProAlaAlaProCysGlyCys 114
Db 214 GGTGTCCCGGGCTGTGGCGCCATGGAGCACAGTGTCCCGCCG---CTGGCGTGTG 270
Qy 115 GluArgLeuValLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGly 134
Db 271 GAGCGCTGTGTCAACGTGGCGGGTGGCTTGAACCCCGCGCGGACAGCTCGG 330
Qy 135 ArgPheProAspThrLeuLeuGlyAspProAlaArgArgGlyArgPheTyrAspAla 154
Db 331 CCGTCCCGGACACGCTGCTGGGGGACCGGAGCGCGGAGCGGCTTCAACGAGCGG 390
Qy 155 ArgArgGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyr 174
Db 391 CGCGCGAGTATTTCTTCAACGACACCGGCGCCAGCTTGATGGTGTCTTAATCTAC 450

QY	175	GLIERGLYGLYARGLEUARGARGPROALAHISVALPROLEUASPYALPHETUDLNU	194
Db	451	CAGTCGGGGCGGGCGGTGAAGACGGGGCGACAGTCCCTCGAGCTCTTCTGGAGAG	510
QY	195	VALALAPHERYGLYLEUGLYALALALALALALALARGLEUARGSLUNASPLUNGLYCS	214
Db	511	GTGTCCTCTACAGGGGTGGGG--CGGGGGCTGGCGGGCTCGGGAGAGACGAGGGCTGC	567
QY	215	PROVALPROPROGLUNARGPROLEUPROVALARGALAPHALARGLUNLEUTRPLEUEN	234
Db	568	GGGGTC--GCCGAGGGCGCGTGGCC--CCGCCCTTGGCCGTCAGCTCGGCTGCTC	621
QY	235	PHGLIUNHEPROGLUSERSERGINALALALARGVALLEUALVALVALSERVALLEUAL	254
Db	622	TTTCGAATTTCTGAGAGCTGCGAGCGTGGCGGGCTGCTGGCTGTCTCGTACTGCTC	681
QY	255	ILEUVALSERILEVALVALPHEYCSLEUGLUTHIRLEUPROASPHEARGASPARG	274
Db	682	ATTCGGTCTCCATCGTGGTCTTTTGCCTCGAGACACTCCAGACTCCGACGACGACGC	741
QY	275	ASPLGYTHRGLYLEUALALALALALALALAGLPROVALPHEPROLABPROLEUN	294
Db	742	GATACCCGGGGCTCGGGCCGGTAGGGGGCTACTGCTCGTCTCGCCGACTGAT	801
QY	295	GLYSESERGINMETPROGLYASNPROPROARGLEUPROPHASNAPROPHENVAL	314
Db	802	GGCTTCAGTCCCATGCCAGGAGGCCCTCCCGACACCTCTCACAGATCATTTCTTG	861
QY	315	VALGLUTHIRLEUCYSLIECYSTRPHESERPHEGLIUNLEUVALARGLEUVALYCS	334
Db	862	GTGAGAGCCCTGTGTACTCTGTCTGTCTTGTGACCTCTGGATCATTTCTGGCTGC	921
QY	335	PROSERYSLALALPHEPHELYASNVALMETASLEULASPHENVALALILEU	354
Db	922	CTTGACAAAGCTGTCTTCTCAAGAAATGTATGAACCTAATGACTCTCGGCATCTG	981
QY	355	PROTYRPHENVALALALEUGLYTHRGLLEUALARGLARGLYVALGLYGLINLAA	374
Db	982	CCTTACTCTGGGCCCTGGGGCAGGGATGACCCGGGCACGGGGGTGGGGCAGCCGCT	1041
QY	375	METSERLEUALALILEUALARGVALILEARGLEUVALARGVALPHEARGLLEPHEYSLEU	394
Db	1042	ATGTCCTGGCCCATTCCTAAGGGTCATCCGATTTGGTGGCTCTCCGCACTTCCAAGCTC	1101
QY	395	SERARGHISERYSLYLEUGLINILEUGLYGLINTHIREUARGLASERMETARGLU	414
Db	1102	TCCAGGACTTCGAAGGGCTGTACAGATCTGGGCACAGACCTCGGGCTCCATGGGTGAG	1161
QY	415	LEUGLYLEUENILEPHELEUPHEILEGLYVALLEUENPHESESERLALVALYR	434
Db	1162	CTAGGTCCTCCATCTTCTCTCTTCATTGGGTGGTCTCTTTCCAGGCCAGCTCAC	1221
QY	435	PHEALAGLUVALASPARGVALASPERHISPHETHSERILEPROGLUSERPHEPTRP	454
Db	1222	TTTGCTGAAGGAGCGGGHAGAACACCACTTTCACAGCATCCCGAGTCTTTTGGTGG	1281
QY	455	ALAVALVALTHRMETINTHRVALGLYTRYGLYASPMETALABROVALTHRVALGLY	474
Db	1282	GCAATGTGCACCATGACACGAGGTGGCTAAGGGACATGGACCCCTGCATCCGTGGGTGC	1341
QY	475	LYSLILEVALGLYSERLEUCYSALALEAGLYVALLEUTHIRLESERLEUPROVALPRO	494
Db	1342	AAGATCGTGGGCTTCTGTGTCATTGCAGGGTGTCTCAACATCTCTGTGCTGGCT	1401
QY	495	VALILEVALSERASNPHESERTYRPHETYNHISARGLUTHIRGLUNGLYGLINLAA	514
Db	1402	GTCAATTGCTCTACTTACTTACTTACTTACACCGGAGACAGAGGGCGAAGAGCAGGG	1461
QY	515	METHESERHISVALASPMETGLNPROCYGLYPROLEUGLUNGLYSLASLANSGLY	534
Db	1462	ATGTACACCACTTGTGGACACACAGCCCTGGGTGATCCCTGGAGGGCAAGGCTAATGGGGG	1521

QY	555	LeuValThrGluVal	559
Db	1522	CTGGGGAGCTGTGAGGGCCCTGAACCTCTCCACCACTCTGGCCCCCTGCAGGAAACAC	158
QY	555	LeuValThrGluVal	559
Db	1582	ATGTGACTGAGGTG	1596
RESULT 7			
US-09-993-811-5			
Sequence 5, Application US/09993811			
Patent No. US20020119476A1			
GENERAL INFORMATION:			
APPLICANT: Pharmacia AB			
TITLE OF INVENTION: Nucleotide Sequences			
FILE REFERENCE: 00248			
CURRENT APPLICATION NUMBER: US/09/993,811			
CURRENT FILING DATE: 2001-11-16			
NUMBER OF SEQ ID NOS: 13			
SOFTWARE: PatentIn version 3.0			
SEQ ID NO 5			
LENGTH: 3473			
TYPE: DNA			
ORGANISM: Mus musculus			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (262)..(1860)			
PUBLICATION INFORMATION:			
DATABASE ACCESSION NUMBER: GenBank/NM_010596			
DATABASE ENTRY DATE: 2000-01-25			
US-09-993-811-5			
Alignment Scores:			
Pred. No.:	2.56e-151	Length:	3473
Score:	2210.50	Matches:	452
Percent Similarity:	84.77%	Conservative:	10
Best Local Similarity:	82.94%	Mismatches:	62
Query Match:	75.75%	Indels:	21
DB:	10	Gaps:	9
US-09-804-014A-8 (1-559) x US-09-993-811-5 (1-3473)			
QY	21	ThrGlyValAlaGlnSerArgArgGlyValArgArgArgArgArgGlyArgAlaGlyArgAla	40
Db	268	ACAAGAAAGCTCAAGACATCCACGGA-----AAAGCGCGGGGTGCAGTGTTCACA	321
QY	41	SerArgGlnArgAlaArgGlyValArgProValAlaLeuArgProAlaGlyValThrValPro	60
Db	322	GGTGTGGGACAGCGCAGAGGGCGCCCT-----AGCCCGCGGGGTAAACACGCGCC	372
QY	61	ProPheSerArgProSerArgProAlaGlyLeuPheTyrAla-----	74
Db	373	CTCTCCCGCGCGCTGGCGCG-----ACTTTCATGCTATTATTTCACCGCGACAC	423
QY	75	ArgThrProAspThrGlyHisArgAlaGlyAlaAlaValGlyAlaThrArgGlyPheAla	94
Db	424	CGGACACCGCGACTGGGGT-----GGCTGCGCGCGCTGCGGCGCACACACGCTTCACC	474
QY	95	GlyArgArgGlyCysAlaArgHisGlyAlaAlaValProAlaAlaProCysGlyCysCys	114
Db	475	GGTCCCGCGCGCTGGCGCGCATAGGACCCAGGTGGCCCGCGCG-----CTGCGCTGTCG	531
QY	115	GluArgLeuValLeuAspValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGly	134
Db	532	CAGCGCGCTGTGCTCAACGTGGCGCGGTGGCGCTTCAGACAGCCGCGCGCACGCTGGC	591
QY	135	ArgPheProAspThrLeuLeuGlyAspProAlaArgArgGlyArgPheTyrAspAspAla	154
Db	592	CGCTTCCCGGACACGCTCTGGGGACCCGGGTGCGCGCACACGCTTCTAGACAGCGCG	651
QY	155	ArgArgGlyValTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyrTyr	174
Db	652	CGCGCGGAGTATTTCTTGACCGACACCGCGCGAGCTTCGATGGGGTCTTACTACTAC	711

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QY 175 GlnSerGlyArgLeuArgArgProAlaHisValProLeuAspValPheLeuGlnGlu 194
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Db 712 CAGTCGGGGGGCGGCTGAGACGGCGGCGACGTCCTCGACGCTCTTCCGAGGAG 771
QY 195 ValAlaPheArgGlyLeuGlyAlaAlaAlaLeuAlaArgLeuArgGluAspGlnGlyCys 214
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Db 772 GTGTCTCTTACGGGGCTGGGG---CGGCGGCTGGCGCGGCTGGGGAGGACGAGGCGCTGC 828
QY 215 ProValProProGluArgProLeuProAlaArgAlaPheAlaArgGlnLeuTrpLeuLeu 234
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Db 829 GCGGTC---GCCGAGCGGCGGCTGGCC---CCGCCCTTGGCGGCTGAGCTGGCTGCCTC 882
QY 235 PheGluPheProGluSerSerGlnAlaAlaArgValLeuAlaValAlaValSerValLeuVal 254
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Db 883 TTCGAATTCCTGAGAGCTGCGAGGCTGCGCGGCTGCGCTGCGCTGCTCCGACTCGTC 942
QY 255 IleLeuValSerIleValValPheCysLeuGluThrLeuProAspPheArgAspAspArg 274
|||||
Db 943 ATCCGTGCTCCATGCTGGTCTTTTTCCTCGAGACACTGCGACACTTCCGCGACGACCG 1002
QY 275 AspGlyThrGlyLeuAlaAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsn 294
|||||
Db 1003 GATGACCCGGGGCTCGCGCGGCTGAGCGGCTGACTGCTGCTCCCTCGCTCGCTCAAT 1062
QY 295 GlySerSerGlnMetProGluAsnProProArgLeuProPheAsnAspProPheVal 314
|||||
Db 1063 GGCTCCAGTCCCATGCGCAGAGACCCCTCCCGCAGACCTTTCACAGATCATCTTTTG 1122
QY 315 ValGluThrLeuCysIleCysTrpPheSerPheGluLeuLeuValArgLeuLeuValCys 334
|||||
Db 1123 GTGGAGACCCCTGTATCGCTGCTCTCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGC 1182
QY 335 ProSerIleAlaIlePhePheLysAsnValMetAsnLeuIleAspPheValAlaIleLeu 354
|||||
Db 1183 CCGAGCAAGGCTGTGTTCTTCAAGAAATGATGAACCTAATGACTTCGGGCAATCCG 1242
QY 355 ProTyrPheValAlaLeuGlyThrGluLeuAlaArgGlnArgGlyAlaGlyGlnGlnAla 374
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Db 1243 CCTTACTTGTGGCCCTGGGCGACGAGTTAGCCCGGACGCGGCTGGGCCCGCGGCT 1302
QY 375 MetSerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgIlePheLysLeu 394
|||||
Db 1303 ATGTCCCTGGCCATCTTAAGGAGTCATCCATGCTGCTGCTTCCGCAATCTTCAAGCTC 1362
QY 395 SerArgHisSerLysGlyLeuGlnIleLeuGlyGlnThrLeuArgHisSerMetArgGln 414
|||||
Db 1363 TCCAGGCATTCGAGGGGCTTACAGATCTTGGGTCAAGACACTGCGGCTTCCATGCGTGA 1422
QY 415 LeuGlyLeuLeuIlePhePheLeuPheIleGlyValValLeuPheSerSerAlaValTyr 434
|||||
Db 1423 CTAGGCTCTGCTATCTTCTCCCTTCATTTGGGCTGCTCTTTCCAGCGAGCTGAC 1482
QY 435 PheAlaGluValAspArgValAspSerHisPheThrSerIleProGluSerPheTrp 454
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Db 1483 TTTGCTGAAGTGAGCGGGGTGACACCATTCACAGATCCCGGAGTCTTTTGCTG 1542
QY 455 AlaValValThrMetThrThrValGlyTyrGlyAspMetAlaProValThrValGlyGly 474
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Db 1543 GCAAGTGTAACCTGACACCGGTTGGCTTATGGGACATGGACCCGTCACCGTGGGTGC 1602
QY 475 LysIleValGlySerLeuCysAlaIleAlaGlyValLeuThrIleSerLeuProValPro 494
|||||
Db 1603 AAGATGTGGGCTCTGTGTGTCATTTGCAAGGTGCTCACCATCTCTGCTGCTGCTG 1662
QY 495 ValIleValSerAsnPheSerTyrPheTyrHisArgGluThrGluGlyGlnGlyAlaGly 514
|||||
Db 1663 GTCATTTGCTCTAACTTGTACTTTTACACCGGAGACAGAGGCGGAGGAGGAGG 1722
QY 515 MetPheSerHisValAspMetGlnProCysGlyProLeuGlnGlyLysAlaAsnGlyGly 534
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Db 1723 ATGTACAGCAATGTGAGACACAGCCCTGGGGTACCTGGAGGGCAAGGCTAATGTGGGG 1782
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QY 535 LeuValAspGlyGluValProGluLeuProProLeuTrpAlaLeuProArgGlnHis 554
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Db 1783 CTGGTGACTCTGAGGTGCTGATCTTCCACGACCTCTGGGCCCTCGACAGAAACAC 1842
QY 555 LeuValThrGluVal 559
|||||
Db 1843 ATGTGATCTGAGGTG 1857

RESULT 8
US-09-954-456-1227
; Sequence 1227, Application US/0995456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1227
; LENGTH: 2867
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1227

Alignment Scores:
Pred. No.: 3,58e-96 Length: 2867
Score: 1447.50 Matches: 338
Percent Similarity: 61.31% Conservative: 63
Best Local Similarity: 49.61% Mismatches: 148
Query Match: 49.61% Indels: 107
DB: 10 Gaps: 20

US-09-804-014a-8 (1-559) x US-09-954-456-1227 (1-2867)
QY 2 GluArgArgArgThrGlySerArg-----ArgGlnLysAspGlyGlnLysGly 17
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Db 34 GAGAGGCAAGAGACGAGGAGCGCGGCGGAGGCTGAGACGAGCTGACGCC 153
QY 18 Asp-----ProGlyThrGlyLysAlaGln-----Ser 26
|||||
Db 94 CAGCAACCCCAAGCTCTCCCAAGAGAGGGGCGCGGAGGCTGAGACGAGCTGACGCC 153
QY 27 ArgArgGlyArgArgArgArgArgGlyArgAlaGlyArg---AlaSerArgGlnArgAla 45
|||||
Db 154 AGCGCCCGCCGCGCTGAGTGGGGGCGCGGAGCGGCTGAGCGGCGGCGGCGGCGGCGG 213
QY 46 -----ArgGlyArgProValAlaLeuArgProAla-GlyValThrValProPro 62
|||||
Db 214 CTCTGCTCCCGCCCATGAGATGCGCTGTCGCTGCGCTGAGACAGCGGCTGCTATGACC 273
```


OY	62	oSer-----	-Arp	ProSerAtrp	ProAlaGlyLeu	Phe	tyrAla	Arg	Phe	ProAs	78
Db	274	GTCAAGAGAGCCGATGAGGCCCGGGCCAGCTGGCCAGCCACAGGGGAGAGCTCCAG									333
OY	78	pThrGlyHisArgAlaGlyAlaAlaVal									-GlyAlaThr 90
Db	334	TGTCGCCCGAGCGCTGGGCTGGAGGATGGGCCCAAGAGCGGGCGCCAAAGGGCGCGGGC									393
OY	90	rArgArgPheAlaGlyArgArgGlyCys									99
Db	394	GCGCAGAGAGAGCGCGAGCTCGGGAGTGGCGCCCTTGCCCTCGCTGGCGGACCCGGAGTGG									453
OY	100	-----									-Al 100
Db	454	CGGCGCTTCGCTCCGCTGCCAGAGAGAGCTCCACGGCTCCAGCGCTCCCGAGAGAC									513
OY	100	aArgHisGlyAlaAlaValProAla									-Al 109
Db	514	GAGGAGAGAAAGAGCGATCCCGGCTGGGACCGTGGAGAGACCAAGGCTCGGGCAGCGGG									573
OY	109	aProGlyGlyCysCysGluArgLeuValLeuAsnValAlaGlyLeuArgPheGlyThrArg									129
Db	574	TCCCTGC---ACGAC-CAGGCGCTCCACATCAACATCTCGGCTGGCTTGGAGACGA									629
OY	129	GAlaArgPheLeuGlyArgPheProAspThrLeuGlyAspProAlaArgArgGlyArg									149
Db	630	GCTGGGCGCCAGCGCGCATGTTCCCAACACATCTCTGGGGGACCCGCGCAAGGCGCTGCC									689
OY	149	gPheArgAspArgAlaArgArgGlyArgPhePheAspArgHisArgProSerPheAspAl									169
Db	690	GTACTGCAACCCCTGAGGAAAGAGTACTTTCGACCCGACACCGGCCACGCTTCCAGCG									749
OY	169	aValLeuArgTyrTyrGlnSerGlyGlyArgLeuArgArgProAlaHisValProLeuAs									189
Db	750	TATCTCTACTACTACCAAGTCCGGGGCGCCCTCGCGAGCGCGATCAAGCTCTCCCTGGA									809
OY	189	pValPheLeuGlnGlyAlaAlaPheTyrArgGlyLeuGlyAlaAlaAlaLeuAlaArgLeuArg									209
Db	810	CGTGTCGCGGAGAGATACCTCTTCCACAGCTGGGGGAGGAGCGCATGGAGCGCTTCGG									869
OY	209	gGluAspGlnGlyCysProValProProGluArgProLeuProArgArgAlaPheAlaArg									229
Db	870	CGAGATAGAGGCTTCATTAAGAAGAGAGAAAGCCCTGCTCCGACAGATTCACAGCG									929
OY	229	gGlnLeuTrpLeuLeuPheGluPheProGluSerSerGlnAlaAlaArgValLeuAlaVal									249
Db	930	CCAGGTGGGCTTATCTTCGAGTATCCGAGAGAGTGGGTGGCGGGGCGCATCGCCAT									989
OY	249	lValSerValLeuVallLeuValSerlLeuValPheCysLeuGlnThrLeuProAs									269
Db	990	CGTCTCGGTCTTGGTATATCCCATCATCATCATCACTTCTGCTGGAGACCTCGCTCGA									104
OY	269	pPheArgAspArgPheArgPheGlyThrGlyLeuAlaAlaAlaAlaAlaGlyProValPhe									289
Db	1050	GTTCAAGGATTAACGTGAGCTGCTCGGCCACCTCGGGCGGCCCCACACAGCTCCGCG--									1100
OY	289	eProAlaPro---LeuAsnGlySerSerGlnMet-----ProGlyAsnPro-----									303
Db	1108	-CCGCGCCCTGGGGCCAAAGCGACCGGGGATCATGGCCCGCCCTTGCGCCCTACGGTGGC									1166
OY	304	-ProArgLeuPro-----PheAsnAspProPhePheValAlaGlyThrLeuCysIleCys									321
Db	1167	ACCGCTCTGCTCCAGAGACCTCGGCGCACCTTCTTCATGT									

Db	1347	CACGGAAGTGGCAGACGACAGCCAGGGCGGAGGAGGCCGCACGATGGGCAAGACC	
OY	374	aMetSerLeuAlaIleLeuArvAlIleArgLeuValArvAlaPheArgIlePheTySle	394
Db	1407	CATGTCCTGGCCATCTCTCCGAGTCAATCCGCGGTGGGGTGTTCCGATCTTCAACT	1466
OY	384	uSerArHisSerTySleUcniInIleuEnglyInThrLeuArGaIlaSerMetArGI	414
Db	1467	CTCCCCGACACTCCAAGGGCGCTGCAGATCCCGGGCAAGACCTTGCAGGCTCCATGAGGA	1526
OY	414	uLengLyLeuLeuIlePhePheLeuPheIleGlyValIleLeuPheSerSerAlaValTy	434
Db	1537	GCTGGGGCTGTCACTCTCTCTCTCATCGGGGTCATCCCTCTCCAGTGGCCGTCTA	1586
OY	434	rPheAlaGlValAlaSpArgValAlaSpSerHisPheThrSerIleProGluUserPheTPR	454
Db	1587	CTTGGCAGAGGCTGCACAACAGGGAACCATTTCTGTACATCCCTGACGCTTGTGCTG	1646
OY	454	pAlaValValThrMetThrThrValGlyTyrglyAspMetAlaProvalrThrValGlyI	474
Db	1647	GGCAGTGTGTACCTATGCACCTGTGGGCTACGGGGACATAGAGGCCATACGTGTGGGG	1706
OY	474	ylysIleValGlySerLeuTySAlaIleAlaGlyValIleuThrIleSerLeuProValPr	494
Db	1707	CAAGAATGCTGGGCTGCTGTGTCCATCGCGGGGTCTCACATTGCTCCGTGTGCC	1766
OY	494	oValIleValSerAnPheSerTyPheTyrHisArgIuThrngIuglyGluLuAlaGI	514
Db	1767	CGTCATGCTGTCCCAACTTCAACTACTTCTACACACCGGGAAGGATCACAGAGAACCGGC	1828
OY	514	yMetPheSerHis-----ValaspMetGlnProCysgly-----Pr	526
Db	1837	AGTCTTAAGGAAGACGACGAGGCACCTACAGACCAGG-GCCGGGGCTGCAGACAGATGCC	1885
OY	526	oLengGlytyrSylasnsnIlglyLeuVal-----AspGlyGluVa	540
Db	1886	AGCGGAAGGTACGGGGAGCAGGAGGATCTTGTGCAAGGCTGGGGGAGACCTTGAGAAATG	1945
OY	540	IProGluLeuProProLeuThrPalapProProArgIu	553
Db	1946	CAGACAGTCCCAGGAGGG---CAGCTGCCCTTACAGAA	1982
RESULT 9			
	US-09-880-107-2354		
	: Sequence 2354, Application US/09880107		
	: Patent No. US20020142981A1		
	: GENERAL INFORMATION:		
	: APPLICANT: Horne, Darci T.		
	: APPLICANT: Vockley, Joseph G.		
	: APPLICANT: Scherf, Uwe		
	: APPLICANT: Gene Logic, Inc.		
	: TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer		
	: FILE REFERENCE: 44921-5028-WO		
	: CURRENT APPLICATION NUMBER: US/09/880,107		
	: PRIOR FILING DATE: 2001-06-14		
	: PRIOR APPLICATION NUMBER: US 60/211,379		
	: PRIOR FILING DATE: 2000-06-14		
	: PRIOR APPLICATION NUMBER: US 60/237,054		
	: PRIOR FILING DATE: 2000-10-02		
	: NUMBER OF SEQ ID NOS: 3550		
	: SOFTWARE: Patentin Ver. 2.1		
	: SEQ ID NO 2354		
	: LENGTH: 2867		
	: TYPE: DNA		
	: ORGANISM: Homo sapiens		
	: FEATURE:		
	: OTHER INFORMATION: Genbank Accession No. US20020142981A1 M55513		
	US-09-880-107-2354		
Alignment Scores:			
Pred. No.:	3,58e-96	Length:	2867
Score:	1447.50	Matches:	338

Db	1592	TGCTTCCTCCAGGCTGGTAAAGTTTGTGAGAGATCCCTGAGAAATTTTCAAGCTTCACCCGCCA	1651
Qy	397	sSerLygLyLeuGlnIleLeuGlyGlnThrIleuArGalaSerMetArgGluLeuGlyLe	417
Db	1652	TTTTGTAGGTCGTGAGGTCCTTGGACATGCTCTTGCAGCTAGTACTAAATGAATTTTCT	1711
Qy	417	uLeuIleAhrPheLeuPheMetIleGlyValValLeuPheSerSerAlaValTyrPheAlaG	437
Db	1712	GCTATATATTTTCCGTGGCTGTAGAGATTTTGGATATTTGCTACCATGATCTTACTATAGCCGA	1771
Qy	437	uValAspArgVal-----AspSerHisPheTh	446
Db	1772	G-----AGAGTGGGACCTCAACCTTACACACCCCTTCAGCTAGTACGACACACACTTCA	1825
Qy	446	rSerIleProGluSerPheThrTptAlaValAlaThrMetThrThrValGlyTyrGlyAs	466
Db	1826	AAACATTTTCCATTTGGGCTTCGTGGGCTGTAGTACCATGATACCTCGGCTATAGGGGA	1885
Qy	466	pMetAlaProValThrValGlyLysIleValGlySerLeuCySAIleAlaGlyVa	486
Db	1886	TATATTACCCCAAAACATGCTGACGAGCATGCTGGTGGAGCCGTGTGCTGTGGCGAGT	1945
Qy	486	lLeuThrIleSerLeuProValProValIleValSerAsnPheSerTyrPheTyr	504
Db	1946	GCTGACATATGACATGCGCACTGCGCTGTCTCATTTGTTCATATTTTGGAAATGACTAC	2000
RESULT 11			
US-10-062-879-3			
: Sequence 3, Application US/10062879			
: Patent No. US20020127649A1			
: GENERAL INFORMATION:			
: APPLICANT: Cockett, Mark I.			
: APPLICANT: Dilks, Daniel W.			
: APPLICANT: Chang Ling, Hsui-Ping			
: APPLICANT: Sokol, Patricia T.			
: TITLE OF INVENTION: Human Potassium Channel Polynucleotides and			
: FILE REFERENCE: ahp-98089			
: CURRENT APPLICATION NUMBER: US/10/062,879			
: CURRENT FILING DATE: 2002-01-31			
: PRIOR APPLICATION NUMBER: US/09/178,109			
: PRIOR FILING DATE: 1998-10-23			
: NUMBER OF SEQ. ID NOS: 4			
: SOFTWARE: PatentIn Ver. 2.0			
: SEQ ID NO 3			
: LENGTH: 2064			
: TYPE: DNA			
: ORGANISM: human			
US-10-062-879-3			
Alignment Scores:			
Pred. No.: 3.02e-44			
Score: 728.00			
Percent Similarity: 51.92%			
Best Local Similarity: 35.63%			
Query Match: 24.95%			
Db:	12	Gaps:	15
US-09-804-014A-8 (1-559) x US-10-062-879-3 (1-2064)			
Qy	74	AlArGrThrProAspThrGlyHisArgAlaGlyAlaAlaValGlyAlaThrArg-ArgPh	93
Db	22	GCCTGCTGCTGCTGAGCTGCCGCGGCTGCCGCCCAAGCATGCTGAGTACCATGCGGCC	81
Qy	93	eAlaGlyArgArgGlyCys-----AlaArgHisGlyAlaAlaValPr	107
Db	82	GGAGTTCGGGCTGCGCTGCTTTTGGCCGGGCTCGCGGCATCGGGATGCGCGGTGCC	141
Qy	107	oAlaAlaProCys-----GlyCysGlyArgLeuVa	118
Db	142	AACGTGCCCATGCTCCCTGCGCCCGCGCCGACAAAGAACACGCGCAG-GATGAGCTGATTGT	200
Qy	118	lLeuAsnValAlaGlyLeuArgPheGlnThrArgAlaArgThrLeuGlyArgPheProAs	138

[illegible]

Db 1179 ATACGAGACATGGTCCCTAAGACGATTGCGAGGAGATCTTGCGCTCATCTGCTCTT 1238
QY 483 eAlaGlyValLeuThrIleSerLeuProValIleValSerAsnPheserTyrPh 503
Db 1239 GAGGGGGCTGCTGATTCATGCTCCGCGACGTCCTGATGTTTCCAACTTATACCGGAT 1298
QY 503 eTyrHisArg-----GluThrGluGlyGluAlaGlyMetPheserH 518
Db 1299 TTACCCACCAAGATCAGACGCTGATTAACGACGAGGCAAAAGAGCCGCTTGCCAG 1358
QY 518 sValAspMetGlnProCysGlyPro-----LeuGluGlyLysAlaAsnGlyL 534
Db 1359 GATCCGCTGCGCAAAACAGGACGATTGCATGCTACCTGCACGACGACGACGCGGCT 1418
QY 534 yLeuValAspGlyGluValProGluLeuProProProLeuThrAlaProProArgL 554
Db 1419 CCTC-----AAGGAGCGCTGAGCTG-----ACGGGACCCCGACAGAGAGACA 1463
QY 554 sLeu 555
Db 1464 CATG 1467

RESULT 12
US-10-062-879-1
; Sequence 1, Application US/10062879
; Patent No. US20020127649A1
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dikls, Daniel W.
; APPLICANT: Chang Ling, Hual-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polypeptides and
; TITLE OF INVENTION: Polypeptides and Uses Therefor
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/10/062,879
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/178,109
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2121
; TYPE: DNA
; ORGANISM: human
US-10-062-879-1

Alignment Scores:
Pred. No.: 3,12e-44 Length: 2121
Score: 728.00 Matches: 186
Percent Similarity: 51.92% Conservative: 85
Best Local Similarity: 35.63% Mismatches: 172
Query Match: 24.95% Indels: 80
DB: 12 Gaps: 15

US-09-804-014a-8 (1-559) x US-10-062-879-1 (1-2121)

QY 74 AAlaArgThrProAspThrGlyHisArgAlaGlyAlaValAlaGlyAlaThrArg-ArgPh 93
Db 22 GCTGGTGGCTTACGCTCGCGCGCGCTGCGGCCCAAGAGCTGAGACCATGCGCGCC 81
QY 93 eAlaGlyValArgArgGlyCys-----AlaArgHisGlyAlaAlaValPr 107
Db 82 GGAATGGGGCTGCTGCTGCTTTTGGCCCGGCTGCGGCATCGGGTGGATGCCGCTGCC 141
QY 107 oAlaAlaProCys-----GlyCysCysGluArgLeuVal 118
Db 142 AACTGCCCATGCCCTGCGCGCGCGCGACAGACAAAGACGCGCAG-GATGAGCTGATGT 200
QY 118 lLeuAsnValAlaGlyLeuAlaArgPheGluThrArgAlaArgThrLeuGlyArgPheProAs 138
Db 201 CCTACAGCTGAGTGGCGGAGGTTCCAGACCTGGAGACCGCTTGAGCGCTTACCGCGA 260
QY 138 pThrLeuLeuGlyAspProAlaArgArgGlyArgPheTyrAspAspAlaArgArgGlyT 158

Db 261 CACCCCTGCTGGCGAGC---ACGGAGAGAGATTCTTTTACAGAGAGACACAGAGCTA 317
QY 158 rPheAspArgHisArgProSerPheAspAlaValLeuTyrTyrGlnSerGlyL 178
Db 318 CTTCCTGACGGGAGCCCGAGGTGTTCCGCTGCTCAACTTACCGCAGC---GG 374
QY 178 yArgLeuAlaArgProAlaHisValProLeuAspValPheLeuGluValAlaPheT 198
Db 375 GAAGCTGCACCTACCCGCGCTACAGAGTGCATCTGCTACGACGACGAGCTGCTTCTA 434
QY 198 rGlyLeuGlyAlaAlaAlaLeuAla-----ArgLeuArg 209
Db 435 CGGCATCTCCCGAGATCATCGGGGACTGCTGCTACGAGAGTACAGACCGCAGAG 494
QY 209 gGlu-----AspGluGlyCysProValProProGluArgProLeuPr 223
Db 495 GGAGACGCGGAGCGGCTCATGACGACACAGACTCGGAGACACAGAGAGTCCATGCC 554
QY 223 oArgArgAlaPheAlaArgGlnLeuThrPheLeuPheGluPheProGlnSerGlnAl 243
Db 555 CTCGCTGAGCTCCGCGACGACCATGTCGCGGCTTGCAGAACCCACACACACAGCT 614
QY 243 aAlaArgValLeuAlaValAlaSerValLeuValIleLeuValSerIleValValPheC 263
Db 615 GGGCTGCTGCTTCTTACTACGTGACTGCTTCTTATGCTGCTGCTATCACCACAGT 674
QY 263 sLeuGluThrLeuProAspPheArgAspAspArgAspGlyTyrGlyLeuAlaAlaAla 283
Db 675 GGTGAGACGGTGCCG-----TGGCGGACG----- 699
QY 283 aAlaAlaGlyProValPheProAlaProLeuAsnGlySerSerIleMetProGlyAsnPr 303
Db 700 -----GTCCCGGAGACAGAGAGTGCCTGCGGGA 731
QY 303 oProArgLeuProPheAsnAspProPhePheValIleGluThrLeuGlySerTyrPh 323
Db 732 G-----CGTACTCGGTGGCTTCTTCTGCTGACAGCGGCTGCTCATGATCTT 782
QY 323 eSerPheGluLeuLeuValAlaArgLeuValCysProSerLysAlaIlePhePheLysAs 343
Db 783 CACCGTGAAGTACCTCGCGGCTTCCGCGGCTCCAGCGCGTACCGCTCATGCCAG 842
QY 343 nValMetAsnLeuIleAspPheValAlaIleLeuProTyrPheValAlaLeuGlyThrGl 363
Db 843 CGTCATGACATCATCAGCTGCGGATCATCATCCTTACTACATC-----GGTCTGCT 896
QY 363 uLeuAlaArgGlnArgGlyValGlyGlnAlaMetSerLeuAlaIleLeuArgValIl 383
Db 897 CATGACCAACAGACGAGCGTCCGCGCTTGTCTACAGCTC----- 939
QY 383 eArgLeuValArgValPheArgIlePheLysLeuSerArgHisSerLysGlyLeuGlnIl 403
Db 940 -CGGCTCTCCGCTTCAAGATCTTCAAGTTTCCCGCACATCCAGCGCGCTGCGGAT 998
QY 403 eLeuGlyGlnThrLeuArgAlaSerMetArgGlnLeuGlyLeuLeuIlePhePheL 423
Db 999 CTTGGGCTACACACTGAAGACTGTGCTCGCACTGGGCTTGTCTTCTCTCTCTCATC 1058
QY 423 eIlleGlyValAlaLeuPheSerSerAlaValTyrPheAlaGlyAlaValAspArgVala 443
Db 1059 CATGGCCATCATCTTGTGACATGATGATTTTATGCGAGAGAGGCTCTCGCGCAG 1118
QY 443 rHisPheThrSerIleProGlnSerPheTyrPheAlaValAlaValThrMetThrValGl 463
Db 1119 CAAGTTCACAGCATCCCTGCTGTTTGGTATACCATCTGTCACCATGACACATGCGG 1178
QY 463 yTyrGlyAspMetAlaProValThrValGlyLysIleValGlySerLeuCysAlaIl 483
Db 1179 ATACGAGACATGGTGCCTTAAGACGATTGACGGGAAAGTCTTCCGCTCATCTCTCT 1238
QY 483 eAlaGlyValLeuThrIleSerLeuProValProValIleValSerAsnPheserTyrPh 503

Db 1239 GAGTGGCGCTGCTGATTCATTCGCCAGTCCCTGATGTTTCCAACTTACCGGAT 1298
 QY 503 eTyHhIsArG-----GluThrgluGluGluAlaGlyMerPheSerHl 518
 Db 1299 TTAACCCAGCAATCAGAGAGCTGATTAACGACGAGCAAAAGAGCCCGCTTCCAG 1358
 QY 518 sValAspMetGlnProCysGlyPro-----LeuGluGlyLysAlaAsnGlyGl 534
 Db 1359 GATCCGTGTGGCCAAACAGGAGCTTCGATGCATCTGACACAGCAACGCGACGGCT 1418
 QY 534 yLeuValAspGlyGluValProGluLeuProProProLeuTyrPalaProProArgLuh 554
 Db 1419 CCTC-----AAGGAGCGCTGGAGCTG-----ACGGGACCCCGAAGAGAGAGA 1463
 QY 554 sLeu 555
 Db 1464 CATG 1467

RESULT 13

US-10-024-623-12
 ; Sequence 12, Application US/10024623
 ; Publication No. US20020187524A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtiss, Roy A. J.
 ; TITLE OF INVENTION: 8099, 46455, 54414, 53763, 67076, 67102, 44181,
 ; 67084FL, AND 67084 ALF, HUMAN PROTEINS AND METHODS OF
 ; TITLE OF INVENTION: USE THEREOF
 ; FILE REFERENCE: MNI-214CP
 ; CURRENT APPLICATION NUMBER: US/10/024,623
 ; CURRENT FILING DATE: 2001-12-17
 ; PRIOR APPLICATION NUMBER: US 60/256,240
 ; PRIOR FILING DATE: 2000-12-15
 ; PRIOR APPLICATION NUMBER: US 60/256,588
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: US 60/258,028
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 1917
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1917)
 US-10-024-623-12

Alignment Scores:

Pred. No.: 4.2e-44 Length: 1917
 Score: 725.50 Matches: 197
 Percent Similarity: 49.81% Conservative: 67
 Best Local Similarity: 37.17% Mismatches: 152
 Query Match: 24.86% Indels: 114
 Db: 9 Gaps: 15

US-09-804-014A-8 (1-559) x US-10-024-623-12 (1-1917)

QY 36 ArgAlaGlyArgAlaSerArgGlnArgAlaArgGlyArgProValAlaLeuArgProAla 55
 Db 12 CGAGAACACAGAGAGGTGATCTCAATGTCGGGGACCGCGACGAAACCTACCGCAG 71
 QY 56 GAlValThValProProSerArgProSerArgProAlaGlyLeuPheThyAla--- 74
 Db 72 CACCTCAAGACCTGCTCCGGAACACGCTGCG-----CCTCTTGGCTCTCTCGAGCCGCC 128
 QY 75 ---ArgThProAspThrGlyHisArgAlaGlyAlaAlaValaGlyAlaThrArgArpHe 93
 Db 129 AGGCACTGCTTGACACGCGGGCGGACACAGCTGACGCGCTGCGCCCTCACCTGCGCC 188
 QY 94 AlagIyArgArgGlyCysAlaArgHisGlyAlaAlaValProAlaAlaProCysGlyCys 113
 Db 189 GCCGCCGAG-----AGCGCCCGCTGTGCC----- 215

QY 114 CysGluArgLeuValLeuAsnValaGlyLeuArgPheGluThrArgAlaArgThLeu 133
 Db 216 -----GGGCGAGCGCGCTG 230
 QY 134 GAlArgPheProAspThrLeuLeuGlyAspProAlaArgArgGlyArg-PheryAspAs 153
 Db 231 CTTCGAGGGCGCGCGGACACTGATTCGCCGCGCGAGCGGCGGACGACATCCCGG 290
 QY 153 pAlaArgArgGlyTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTy 173
 Db 291 TGGCGGCGCGGAGTCTTTGACCGGACACCGCGCGCTTCGCTATGCTCAATTA 350
 QY 173 rTyrgInserGlyGlyArgLeuArgProAlaHisValProLeuAspValPheLeuGl 193
 Db 351 CTACCGCACCC---GGCACTGCACTGCCCGAGACGTCGTGCGGCGCTCTCGAGAGA 407
 QY 193 uGluValAlaPheTyrGlyLeuGly----- 201
 Db 408 GGAGCTGGCTTCTGTGGCATCGACGAGACGACGTCGAGCCCTGCTGATGACCTTA 467
 QY 201 ----- 201
 Db 468 CCGGACGACCGCGGACCGCGAGAGCGCTGCATCTTCGAGACCCCGACTTATGG 527
 QY 202 -----AlaAlaAlaLeuAlaArgLeuArgGluAspGl 212
 Db 528 CGGCGACCGCGCGGACGAGAGGACTGGCGGCAAGAGCGTGGCATCGAGAGCGCGG 587
 QY 212 uGlyCysProValProProGluArgProLeuProArgArgAlaPheAlaArgGluLeuTr 232
 Db 588 GGGGCGCGGGGCGCGGACGCAATCTGCGCGTGGAGAGGCTGCAGCCCGCATGTG 647
 QY 232 pLeuValPheGluPheProGluSerSerGlnAlaAlaArgValAlaValaValaSerVa 252
 Db 648 GGCCCTCTGAGAGACCTTACTGTCAGACCGCGAGGTTATGCTTGTCTTCTT 707
 QY 252 lLeuValAlaLeuValSerAlaValaValaPheCysLeuGluThrLeuProAspPheArgAs 272
 Db 708 ATTCTTCATCTCGTTTCAATTAACAATTTTGGCTGGAACACATGAAGCTTCAATAT 767
 QY 272 pAspArgAspGlyThrGlyLeuAlaAlaAlaAlaAlaGlyProValPheProAlaPr 292
 Db 768 TGTAAACAAACAGACA-----GAACCACTC----- 792
 QY 292 oLeuAsnGlySerSerGlnMetProGlyAsnProProArgLeuProPhe-----As 309
 Db 793 -ATCAATGGCACAGTGTGTT-----CTACAGTATGAATGAAC 833
 QY 309 nAspProphePheVal---ValGluThrLeuCysIleCysTrpPheSerPheGluLeuLe 328
 Db 834 GGATCCTGCTGACGTATGTAAGAGAGTGTGTGGTGTGTTTACTTTGAATTTT 893
 QY 328 uValArgLeuLeuValCysProSerLysAlaIlePhePheLysAsnValMetAsnLeuIl 348
 Db 894 ACTCCGATGTGTTTTCACCCCAATAACTGAATTCATCAAAAATCTCTGGAATATCAT 953
 QY 348 eAspPheValAlaIleLeuProTyrPheValAlaAlaLeuGlyThrgLuleuAlaArgGlnAr 368
 Db 954 TACATTTGTGGCATCTCACTTCTTACTTAAGGTGGAGCTCACT----- 999
 QY 368 gGlyValGlyGlnGlnAlaMetSer-----LeuAlaIleLeuArgValAlaArgLeuVa 386
 Db 1000 -GGCGTGTATCCAAAGCGTAAGATGTGTTGGCTTCACAGGTGTGTAGTGTGT 1058
 QY 386 lArgValPheArgIlePheLysLeuSerArgHisSerLysGlyLeuGlnIleLeuGlyGl 406
 Db 1059 GAGGATCTCGAAGAAATTCACACTCACCGCATTTTGTAGCTCGAGGGTCTTGAGCA 1118
 QY 406 nThrLeuArgAlaSerMetArgGluLeuGlyLeuLeuIlePhePheLeuPheIleGlyVa 426
 Db 1119 TACTCTTGAGGTAGTACTAATGAATTTTGTGCTGATTAATTTCTTGCTTGAAGAT 1178
 QY 426 lValLeuPheSerSerAlaValaValaValaValaValaValaValaValaValaVala 441

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Db 1179 TTGATATTTGCTACCATGATCTACTATGCCGAG-----AGAGTGGAGCTCAACCTAA 1232
Qy 442 -----AspSerHisPheThrSerLeuProGluSerPheThrProAl 455
Db 1233 CGACCCCTTCACGCTAGTACGACACACAGTTCCAAAACATTCCCTGGGTCTGGTGGGC 1292
Qy 455 aValaValThMetThrThrValaGlyTyrGlyAspMetAlaProValaThrValaGlyGly 475
Db 1293 TGTAGTACCATGACTACCTCGGTATGGGATATGTACCCCAACATGTCAGGCAT 1352
Qy 475 sIleValaGlySerLeuCysAlaIleAlaGlyValaLeuThrIleSerLeuProValaProva 495
Db 1353 GCTGGTGGAGCCCTGTGTGCTGTGCTGCTGAGTCTGACATAGCATTGCAGTGCCTGT 1412
Qy 495 lIleValaSerAsnPheSerTyrPheTyr 504
Db 1413 CATTGTCAATTAATTTTGGAAATGACTAC 1440

RESULT 14
US-10-016-647-3
; Sequence 3: Application US/10016647
; Patent No. US20020160475A1
; GENERAL INFORMATION:
; APPLICANT: Friddele, Carl Johan
; APPLICANT: Hilbun, Erin
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020160475A1el Human Ion Channel Protein and Polynucleotide
; FILE REFERENCE: LEX-0284-USA
; CURRENT FILING DATE: US/10/016,647
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/257,932
; NUMBER OF SEQ. ID NOS: 3
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1844
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-016-647-3

Alignment Scores:
Pred. No.: 9,14e-39 Length: 1844
Score: 651.50 Matches: 187
Percent Similarity: 48.45% Conservative: 78
Best Local Similarity: 34.19% Mismatches: 161
Query Match: 22.33% Indels: 122
DB: 9 Gaps: 21

US-09-804-014a-8 (1-559) x US-10-016-647-3 (1-1844)
Qy 2 GluArgArgArgThrGlySerArgArgGluLysAspGlyLysGlyAspProGlyThr 21
Db 271 CAGGCGCGGAGATCTGCGAG-----CCAGGCGACC 300
Qy 22 ---GlyLysAlaGlnSerArgArgGlyArgArgArgArgArgGlyArgAla 40
Db 301 CCCGGCCAGCGGAGGCGAGGAGAGCCCGAGGAGCGCGG----- 345
Qy 41 SerArgLysArgAlaArgGlyArgProValaIleLeuArgProAlaGlyValaThrPro 60
Db 346 CCCGAGCGGCGCT----- 360
Qy 61 ProProSerArgProSerArgProAlaGlyLeuPheTyrAlaArgThrProAspThrGly 80
Db 361 CCCCGTCAGCCAGCGGCGAGCGAGCC-----CCGCTGGCGGC 399
Qy 81 HisArgAlaGlyAlaAlaValaGlyAlaThr---ArgArgPheAlaGlyArgArgGlyCys 99
Db 400 TTGGGGTGGGGGCTGACGCGGCGCCCTCGGCGGCGAAAGTCCCGCGGCGCGCAGCCATG 459
Qy 100 -----AlaArgHisGlyAlaAlaAlaValaProAlaAlaProCysGlyCysCysGluArgLeu 117
Db 111 ----- 117
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Db 460 ACCTTCGGGCGCAGCGGCGGCGCC-----TCGGT 489
Qy 118 ValLeuAsnValaAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGlyArgPhePro 137
Db 490 GTGCTGAACGTGGGCGGCGCGCGGATTCGCTGTCCGGAGAGCTGCTGAAGACTTCCCG 549
Qy 138 -----AspThrLeuLeuGlyAspProAlaArgArgLeuArgPhe----- 150
Db 550 CTGGCGCGCGGAGCGCGCTGCAAGCGCTGCCGCTCCAGCGCGCAGCTGCAAGTGTGC 609
Qy 151 -----TyrAspAspAlaArgArgGlyTyrPhePheAspArgHisArgProSerPheAsp 168
Db 610 GAGCACTACGACCGCGAGCGCAACAGACTTCTTCACCGGACCTGAGGCGCTTGGC 669
Qy 169 AlaValaLeuTyrTyrTyrGlnSerGlyArgGluArgArgProAlaHisValaProLeu 188
Db 670 TTCACTCTGCTACGTCGCGCGCGCGCGCAAGCTGCTTCCGCGCGCGGATGTGCGAG 729
Qy 189 AspValaPheLeuGlnGluValaAlaPheTyrGlyLeuGlyAlaAlaAlaLeu----- 205
Db 730 CTCCTCTTCAACAAGAGATGATCTACTGGGGCGCTGAGGGCGCGCAGTCACTGTC 789
Qy 206 AlaArgLeuArgGluAspGlu-GlyCys-----ProValaProGluArgProLeu-- 222
Db 790 TGCAGCGCGCGCTGCGACGAGCGCGATGTCGACACTTCACTTCTACTGCGCGAGAG 849
Qy 223 -----ProArgArgAlaPheAlaAr 229
Db 850 CCGGGCGCTGCGGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCC--TCCAG 908
Qy 229 gGlnLeuTyrPheLeu-----LeuPheGluPheProGluSerGlnAlaAla 244
Db 909 GCGC---TGGCTGAGGCGCATGCGCGGACCTTGAGAGACCCAGCTGCGTGGCGCGC 965
Qy 244 aArgValaLeuAlaValaSerValaLeuValaIleLeuValaSerIleValaPheCysLe 264
Db 966 GCAAGTCTGCGCTGAGCTGCGTGGTGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1025
Qy 264 uGluThrLeuProAspPheArgAspAspArgAspGlyThrGlyLeuAlaAlaAlaAla 284
Db 1026 CAGCAGCTTCCCGACCTGCGCGCAC-----GCAGC 1055
Qy 284 aAlaGlyProValaPheProAlaProLeuAsnGlySerSerGlnMetProGlyAsnProPr 304
Db 1056 GCGCGAC-----AACCGAGC----- 1071
Qy 304 aArgLeuProPheAsnAspProPhePheValaGluThrLeuGlyIleCysTrpPheSe 324
Db 1072 -----CTGATGACCGGAGCAGCATATGAGCTATGCTGATAGGTGTGTCAC 1121
Qy 324 rPheGluLeuLeuValaArgLeuLeuValaCysProSerLysAlaIlePhePheLysAsnVa 344
Db 1122 TGCGAGTGCATCTGTGAGTTGATCTGTCAAAACAAAGCTGAGTTGTCAAGAGACC 1181
Qy 344 lMetAsnLeuIleAspPheValaIleLeuProTyrPheValaAla---LeuGlyTrpG 363
Db 1182 CTTGAACATCTTATATTACGCAATCAGCGCTATATACCTCTGTGTTGATGAGACGT 1241
Qy 363 uLeuAlaArgGlnaArgGlyValaGlyGlnAlaMetSerLeuAlaIleLeuArgVala 383
Db 1242 GTTTACAGCGAGAACTCTCAACTCCAGAGGCTGGA-----GTCACTTGAAGGACT 1295
Qy 383 eArgLeuValaArgValaPheArgGliePheLysLeuSerArgHisSerLysGlyLeuGln 403
Db 1296 TAGAATATGAGGATTTTGGTGGATTAAGCTTGAACCTTCACTTCACTTCACTTCACT 1355
Qy 403 eLeuGlyThrLeuArgAlaSerMetArgGluLeuGlyLeuLeuLeuPhePheLeuPhe 423
Db 1356 ACTGCGTTGACTCTCAACGCTTCTACCGAGAGATGTTATGTTACTTGTCTTCACTTGG 1415
Qy 423 eIleGlyValaValaLeuPheSerSerAlaValaTyrPheAlaGlu-----ValaAs 439
Db 1416 TGTTCATGTCATCTTATGATGACATTCTGACCTTCTGACATGATGGGTGACCTGGA 1475
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